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Run on:	October 26, 2002, 21:05:13 ; Search time 11 Seconds (without alignments) 813.111 Million cell updates/sec		
title:	US-09-840-795-19		
Sequence:	1 MDCQENEWWDOWGRVCVTCR. .... AQLFSLSDSVPIPQQQGPEM 231		
Scoring table:	BLOSUM62		
Searched:	105244 seqs., 38719550 residues		
Total number of hits satisfying chosen parameters:	10524		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing:	Minimum Match 0%		
Database :	Maximun Match 100% Listing first 45 summaries  SUMMARIES		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
Result No.	Query length	DB ID	Description
1	153.5	12.1	TNR7_HUMAN
2	152.5	12.0	P20842 homo sapien
3	145.5	11.4	P50284 mus musculu
4	145	11.4	P119438 homo sapien
5	143.5	11.3	P22118 mus musculu
6	143	11.2	P41277 mus musculu
7	142	11.2	P077736 sus scrofa
8	141.5	11.1	P035305 mus musculu
9	134.5	10.6	Q92955 homo sapien
10	134.5	10.6	P51867 bos taurus
11	134.5	10.6	P50555 sus scrofa
12	134	10.5	O19131 bos taurus
13	132.5	10.4	P36941 homo sapien
14	130	10.2	P20333 homo sapien
15	129.5	10.2	P22934 rattus norv
16	129.5	10.2	P20334 mus musculu
17	124.5	9.8	P25446 mus musculu
18	124	9.7	Q07011 homo sapien
19	122	9.6	Q9yf96 homo sapien
20	121	9.5	O15197 homo sapien
21	119	9.3	Q63199 rattus norv
22	118	9.3	P22445 homo sapien
23	117	9.2	P25119 mus musculu
24	116.5	9.0	Q93038 h wsl-1 pro
25	114.5	9.0	P18519 gallus gallus
26	114.5	9.0	P15725 rattus norv
27	111	8.7	P29823 myxoma virus
28	110.5	8.7	P47741 mus musculu
29	108	8.5	P15215 drosophila
30	108	8.5	Q13444 homo sapien
31	107.5	8.4	P0CK5_MOUSE
32	107	8.4	Q04592 mus musculu
33	107	8.4	Q28203 bos taurus
			Q61789 mus musculu
			P101763 homo sapien
			P25391 homo sapien
			P25391 homo sapien
			P10137 mus musculu
			P25942 homo sapien
			P28908 homo sapien
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DR	SMART; SW00208; TNFR; 2.	RL	Genomics 30:312-319(1995).
DR	PROSTIE; PS00652; TNFR_NGR_1; 1.	CC	-!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
DR	PROSTIE; PS0050; TNFR_NGR_2; 1.	CC	IMMUNE DEVELOPMENT.
KW	T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;	CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
KW	Phosphorylation.	CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
FT	SIGNAL 1 20	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	CHAIN 21 260	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
FT	POTENTIAL.	CC	the European Bioinformatics Institute. There are no restrictions on its
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FT	SUPERFAMILY MEMBER 7.	CC	modified and this statement is not removed. Usage by and for commercial
FT	EXTRACELLULAR (POTENTIAL).	CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ).
FT	TRANSMEM 21 191	CC	or send an email to license@isb-sib.ch).
FT	POTENTIAL.	CC	-----
FT	DOMAIN 213 260	CC	INTERPRO; IPR01368; TNFR_c6.
FT	CYTOSMIC (POTENTIAL).	CC	EMBL; U29173; AA68964..1; -.
FT	TNFR-CYS 1.	CC	EMBL; I38423; AA800846..1; -.
FT	TNFR-CYS 2.	CC	EMBL; U30798; AA81334..1; -.
FT	REPEAT 64 104	CC	HSSP; P25942; ICDF.
FT	TNFR-CYS 3.	CC	MGT; 104875; Ltbr.
FT	CARBHYD 95 141	CC	InterPro; IPR0020; TNFR_c6.
FT	PHOSPHORYLATION (POTENTIAL).	CC	ProDom; PD000771; TNFR_c6..1.
FT	MOD_RES 219 219	CC	SMART; Sm0208; TNFR..3.
FT	A -> T (IN REF. 2).	CC	PROSTIE; PS00652; TNFR_NGR_1; 2.
FT	SEQUENCE 59 59	CC	PROSTIE; PS0050; TNFR_NGR_2; 3.
FT	MW; 43C38B92FA90D4E2 CRC64;	CC	DR
FT	Query Match 12.1%; Score 153.5; DB 1; Length 260;	CC	DR
FT	Best Local Similarity 25.9%; Pred. No. 3e-06; Indels 99; Gaps 18;	CC	DR
FT	Matches 72; Conservative 29; Mismatches 78; Signal 1	CC	DR
FT	Indels 99; Gaps 18;	CC	DR
OY	3 COENEWDDQWGRGVTCORCGPQELSKSDKGCGYEGGDACTACPPRRYKSSWGH--KCQ 59	CC	DR
Db	27 CPERHYWAQKLC-CQMECPGTFLVKDCDQHDK-AQCDPCIP-GVFSFSPDHTRPHCE 82	CC	DR
OY	60 SCITC--AVINRQVKVNCTATSNAVCG---DCLPRFYRKTRIGGLQDOBCIPC-T-QT 111	CC	DR
Db	83 SCRICHNSGLVR---NCATTAACRACRNGWQC-----RDKECTECGPLPN 125	CC	DR
OY	112 PTSEWQCATLS-----LVEA-----DAPTV-----DPAEA..- 137	CC	DR
Db	125 PSLTARSSQALSPLHPQPTILPVSEMLEARHTAGHMQTLADFROLPARTISTHWPPQRSLC 185	CC	DR
OY	138 -----TLVLVSSLLVVFLLAFLQLFFLCKOFFENRHCQRGGLQFEAKTAKESSLFPV 192	CC	DR
Db	186 SSDFTIRLYTFSGMFLVFTA-GALFLHQRY-----RSNKGES--PV 226	CC	DR
OY	193 PPSKETSAFSQVSHAPGSIAQLFSLDSVPIPOQQQGP 230	CC	DR
Db	227 EPA-EPCRVSCPREEGS-----TIPQEDYRKPE 255	CC	DR
RESULT 2		CC	FT
TNFR_MOUSE	STANDARD; PRT: 415 AA.	CC	REPEAT 42 81
ID: TNFR_MOUSE		CC	FT
P:0284;		CC	REPEAT 82 124
DT 01-OCT-1996 (Rel. 34, Created)		CC	FT
DT 01-OCT-1996 (Rel. 34, Last sequence update)		CC	REPEAT 125 170
DT 16-OCT-2001 (Rel. 40, Last annotation update)		CC	FT
DE Lymphotoxin-beta receptor precursor.		CC	REPEAT 171 213
GN LBR OR TNFR OR TNFRSF3.		CC	FT
OS Mus musculus (Mouse)		CC	DISULFID 43 58
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		CC	FT
OC NCBI_TaxID=10090;		CC	DISULFID 59 72
[1] SQUENCE FROM N.A.		CC	BY SIMILARITY.
STRAIN=CVB; TISSUE=Lung;		CC	DISULFID 62 80
MEDLINE=96072804; PubMed=7504541; FORCE W.R., Waiter B.N., Hession C., Tizard R., Kozak C.A., Browning J.L., Ware C.F.; "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression." J. Immunol. 155:5280-5288(1995).		CC	BY SIMILARITY.
RN [2] SEQUENCE FROM N.A.		CC	DISULFID 83 98
RX MEDLINE=9613885; PubMed=8586432; Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S., Honjo T.; "The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping";		CC	BY SIMILARITY.
RP	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 172 187
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 172 187
RP	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 40 40
RN	Indels 89; Gaps 20;	CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
RP	SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;	CC	SEQUENCE 179 179
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 139 150
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 142 169
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 172 187
RN	Indels 89; Gaps 20;	CC	BY SIMILARITY.
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 40 40
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;
RN	Indels 89; Gaps 20;	CC	-----
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
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RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
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RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
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RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB 1; Length 415;	CC	DISULFID 46 46
RN	Best Local Similarity 25.3%; Pred. No. 3e-06; Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Matches 74; Conservative 31; Mismatches 99; Signal 1	CC	DISULFID 46 46
RN	Indels 89; Gaps 20;	CC	DISULFID 46 46
RN	Query Match 12.0%; Score 152.5; DB		

RESULT 3

TRIA\_HUMAN STANDARD; PRT; 455 AA.

ID TRIA\_HUMAN STANDARD; PRT; 455 AA.

AC P19438; DT 01-FEB-1991 (Rel. 17, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tumor necrosis factor receptor 1 precursor (Tumor necrosis factor binding protein 1) (TNF<sub>R1</sub>) (p60) (TNF-R1) (p55) (CD120A).

GN TNFRSF1A OR TNFR1 OR TNFAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TAXID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=90235285; PubMed=2158863;

RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,

RA Gettanaga T., Granger G.A., Lenz R., Raab H., Kohr W.J., Goeddel D.V.,

RT "Molecular cloning and expression of a receptor for human tumor

RT necrosis factor."

RL Cell 61:361-370(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=90235284; PubMed=2158862;

RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,

RA Tabuchi H., Lesslauer W.,

RT "Molecular cloning and expression of the human 55 kd tumor necrosis

RT factor receptor."

RL Cell 61:351-359(1990).

RN [3]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.

RX MEDLINE=9106021; PubMed=169610;

RA Nophar Y., Kempf O., Brakelsbusch C., Engelmann H., Zwang R.,

RA Adenka D., Holtmann H., Wallach D.,

RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF<sub>R</sub>, cloned using amino acid

RT soluble form, encodes both the cell surface and a soluble form of the

RT receptor."

RL EMBO J. 9:3269-3278(1990).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=9109041; PubMed=1702293;

RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,

RA Lantz M., Olson T., Hauptmann R., Stratowa C., Adolf G.R.,

RT "Molecular cloning and expression of human and rat tumor necrosis

RT factor receptor chain (p60) and its soluble derivative, tumor

RT necrosis factor-binding protein."

RL DNA Cell Biol. 9:705-715(1990).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=91017509; PubMed=2170974;

RA Gray P.W., Barrett K., Chanty D., Turner M., Feldman M., Ambros P.F.,

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and

RT expression of recombinant soluble TNF-binding protein."

RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=9225004; PubMed=1315717;

RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.,

RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and

RT localization to chromosome 12p13."

RL Genomics 13:219-224(1992).

RN [7]

RP SEQUENCE OF 41-45.

RX MEDLINE=90110215; PubMed=2153136;

RA Engelman H., Novick D., Wallach D.,

RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface

RT tumor necrosis factor receptors."

RL J. Biol. Chem. 265:1531-1536(1990).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2-85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.

RX MEDLINE=92258609; PubMed=8387891;

RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,

RA Broger C., Loetscher H., Lesslauer W.,

RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF beta complex: implications for TNF receptor activation."

DR Cel1 73:431-445(1993).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.

RX MEDLINE=9094982; PubMed=8939750;

RA Nasimith J.H., Devine T.Q., Khono H., Sprang S.R.,

RT "Structures of the extracellular domain of the type I tumor necrosis factor receptor."

RL Structure 4:1251-1262(1996).

CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTER MOLECULE FADD .

CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYCLOTIDAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACTI SPHINGOMYELINASE.

CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.

CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.

CC -!- DOMAIN: THE DOMAIN THAT INDUCES A SMASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry; WWW="HTTP://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".

CC ---

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CC ---

DR EMBL: X55313; CAA39021.1; --.

DR EMBL: M33294; AAA03210.1; --.

DR EMBL: M60275; AAA36756.1; --.

DR EMBL: M52286; AAA36753.1; --.

DR EMBL: M63121; AAA36754.1; --.

DR EMBL: M73866; AAA61201.1; --.

DR EMBL: M75864; AAA61201.1; JOINED.

DR EMBL: M75865; AAA61201.1; JOINED.

DR EMBL: M60275; AAA36756.1; --.

DR EMBL: A21522; CAA01558.1; --.

PIR: A3489; GOHUTL.

DR PIR: A35010; A35010.

DR PIR: S12057; S12057.

DR PIR; A38208; A38208.

DR PIR; 31-JUL-94.

DR PDB; 1NCF; 07-DEC-95.

DR PDB; 1EXT; 11-JAN-97.

DR MIM: 191190; --.

DR InterPro; IPR00489; Death.

DR InterPro; IPR001368; TNFR\_C6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00220; TNFR\_C6; 4.

DR Prodom; PD00071; TNFR\_C6; 1.

DR SMART; SM00208; TNFR; 4.

DR	PROSITE: PS50050; TNFR_NGFR_1; 3.	DT	16-OCT-2001 (Rel. 40), Last annotation update
DR	PROSITE: PS50017; DEATH_DOMAIN; 1.	DE	Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RL1)
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;	DE	(p55)
KW	3D-structure; Polymorphism.	GN	TNFRSF1A OR TNFR1 OR TNFR-1.
SIGNAL	1	OS	MUS musculus (Mouse).
FT	CHAIN	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
FT	CHAIN	OX	NCBI_TAXID=10090;
FT	DOMAIN	RN	[1]
FT	TRANSMEM	RP	SEQUENCE FROM N.A.
FT	DOMAIN	RX	Medline=9118785; PubMed=1849278;
FT	REPEAT	RA	Lewis M., Tarraglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.
FT	REPEAT	RT	"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific";
FT	REPEAT	RT	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
FT	DISULFID	RL	[2]
FT	DISULFID	RN	SEQUENCE FROM N.A.
FT	DISULFID	RX	Medline=91246168; PubMed=1645445;
FT	DISULFID	RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.
FT	DISULFID	RA	"Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";
FT	DISULFID	RT	Mol. Cell. Biol. 11:3020-3026(1991).
FT	DISULFID	RN	[3]
FT	DISULFID	RP	SEQUENCE FROM N.A.
FT	DISULFID	RX	Medline=91285014; PubMed=1647956;
FT	CARBOHYD	RA	Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissnerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.
FT	CARBOHYD	RT	"Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.";
FT	CARBOHYD	RT	Eur. J. Immunol. 21:1649-1656(1991).
FT	VARIANT	RN	[4]
FT	CONFFLICT	RP	SEQUENCE FROM N.A.
FT	CONFFLICT	RC	TISSUE=Spleen;
SQ	SEQUENCE	RX	Medline=92033815; PubMed=1657756;
Query Match	11.4%; Score 145.5; DB 1; Length 455;	RA	Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
Best Local Similarity	21.3%; Pred. No. 1.7e-05;	RT	"Molecular cloning and expression of the mouse Tnf receptor type b.";
Matches	66; Conservative 36; Mismatches 109; Indels 99; Gaps 14;	RL	Immunogenetics 34:338-340(1991).
OY	3 COENEWMQOWGRCVTTCORCGPQELSKDGYCPEGDAYCTACPPRRVKSWSGH-HKQCSQ 61	RP	SEQUENCE FROM N.A.
Db	44 CPQGKYIHPQNNISICTKCKTYLYNDP-GPGQDTCRCESGSRTASENHLRHCLSC 102	RX	Bebo B.F., Linthicum D.S.; "Nucleotide sequence of the TNF type I receptor from a mouse endotheiloma cell line";
OY	62 ITG-AVTNRVQKVNTATSNAVCGDCLPRFYRK----- 93	RA	Immunogenetics 39:450-451(1994).
Db	103 SKCRKEMQGVETSSCTVDRDYVCG-GRKNQRHYWSENLIFQFCNCSLCLNGTVHLSQKEK 161	RT	Medline=94245292; PubMed=8188324;
OY	94 -----TRIGG-LQDQBCICTKQOPTSEVCAFOQLSLVADAPTPVPOEAT-----L 139	RT	"Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.";
Db	162 QNTVCTCHAGFFLRENVCSCS-----NCKKSLECTKLCLIPOTENVKGTEDSGTIVL 213	RL	Mol. Immunol. 30:165-175(1993).
OY	140 VALVSSL-LWVFTLAFLGFLFLICK--QFFNRHC---QRGGLIQFEADAKTAKERSLF 190	CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUTTS CASPASE-B TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
Db	214 LPLVTFIFGLCLISLFLIGMLRYQRMKSKLYSIVCGKSTPEKELEGITTKPLAPNPSF 273	CC	PROTEIN: TNF-binding to the extracellular domain of TNFR1 leads to homotrimerization. Once aggregated the receptors death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various tradd-interacting proteins such as TRAF, RIP and possibly FADD, are recruited to TNFR1 complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa B signaling (by similarity).
OY	191 -----PVPSKETSAESQVSWAPGS-----LQOLF 216	CC	-1- SUBUNIT: TNF-binding to the extracellular domain of TNFR1 leads to homotrimerization. Once aggregated the receptors death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various tradd-interacting proteins such as TRAF, RIP and possibly FADD, are recruited to TNFR1 complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa B signaling (by similarity).
Db	274 SPTPGTTPLGLGFSPVPSSTFTSS--TTYPEDCPNFAAPRKEVAPPYQGADPILATALLA 330	CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
RESULT	4	CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
TRIA_MOUSE	STANDARD; PRT: 454 AA.	CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
ID	P2518;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
AC	01-MAY-1992 (Rel. 22, Created)	CC	
DT	01-MAY-1992 (Rel. 22, Last sequence update)	CC	

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 CC or send an email to license@isb-sib.ch).

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DR M60468; AAA29751.1; -

EMBL; M59377; AAA40464.1; -

EMBL; X59238; CAN41922.1; -

DR EMBL; X57796; CAN09361.1; -

EMBL; L26349; AA59361.1; -

DR EMBL; M76656; AAA40465.1; -

DR EMBL; M88067; AAA40465.1; JOINED.

DR PIR; A38634; Q0MSN1.

DR PIR; S16677; S16677.

DR PIR; S19021; S19021.

DR HSSP; P19438; TEXT.

DR MGD; MGI:1314884; Tnfrsf1a.

DR InterPro; IPR000488; Death.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00050; TNFR\_c6; 4.

DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.

DR PROSITE; PS0017; DEATH\_DOMAIN; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.

FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 213 235 POTENTIAL.

FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).

FT REPEAT 43 82 TNFR\_CYS 1.

FT REPEAT 83 125 TNFR\_CYS 2.

FT REPEAT 126 166 TNFR\_CYS 3.

FT REPEAT 167 195 TNFR\_CYS 4.

FT DOMAIN 339 349 N-SNAKE ACTIVATION DOMAIN (NSD).

FT DOMAIN 356 441 DEATH.

FT DISULFID 44 58 BY SIMILARITY.

FT DISULFID 59 72 BY SIMILARITY.

FT DISULFID 62 81 BY SIMILARITY.

FT DISULFID 84 99 BY SIMILARITY.

FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.

FT DISULFID 127 143 BY SIMILARITY.

FT DISULFID 146 158 BY SIMILARITY.

FT DISULFID 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 185 195 BY SIMILARITY.

FT CARBOHYD 154 54 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 202 202 R -> G (IN REF. 6).

FT CONFLICT 394 394 AA: 50129 MW: 07102c28C3C2B6d9 CRC64;

SEQUENCE FROM N.A.

RESULT 5 TNR\_MOUSE STANDARD; PRT; 250 AA.

ID TNR\_MOUSE

AC P41272;

DT 01-FEB-1995 (Rel. 31, created)

DT 01-FEB-1995 (Rel. 31, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Tumor necrosis factor receptor superfamily member 7 precursor (CD27L)

DE receptor (T-cell activation antigen CD27).

GN TNFRSF7 OR CD27.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Scurognathi; Muridae; Mus.

OX NCBI\_TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-B6/CBA; TISSUE-Thymus;

RX MEDLINE-9320296; PubMed=8834562;

RA Gravestein L.A., Blom B., Nolten L.A., de Vries E., van der Horst G., Ossendorp F., Borst J., Loenen W.A., "Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte-specific member of the nerve growth factor receptor family.", Eur. J. Immunol., 23:943-950(1993).

RT -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: IN THYMUS AND SPLEEN, BUT NOT IN NON-LYMPHOID TISSUES.

CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.

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CC DR PIR; A49053; R49053.

DR HSSP; P19438; INCF.

DR MGD; MGI:8836; Tnfrsf7.

DR InterPro; IPR00138; TNFR\_c6.

DR Pfam; PF000771; TNFR\_c6; 2.

DR PRODOM; PD000771; TNFR\_c6; 1.

DR SMART; SM0208; TNFR\_2.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PS5050; TNFR\_NGFR\_2; 1.

DR T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 250 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 7.

FT DOMAIN 21 182 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 183 203 CYTOPLASMIC (POTENTIAL).

---

QY 3 CQENEYWDQWGRCVTCQRCGPQELSKDCGEGGDAVCTAGPPRKYKSSWH-HKQSC 61

DP 44 CPGKVWHSKNISCTKCHGTYLVSDCP-SPGRDFTVCREKGFTTAQSQNLRCCL 102

QY 62 RTC-AVINVQVKNTATSNAYCG-----DCLPFRYKTRI----- 96

DB 103 KVKRKEMSQVEISPQCQADKTVGCKKENQFORYLSETHFOCWDCSPCFNGTWIPCKETQ 162

QY 97 -----GG--LQDQEC1PCTKPTSEVQCAFQLSLVEADAPTVPPOEATVALVSSL 147

FT REPEAT 26 63 TNFR-CYS 1.  
 FT REPEAT 64 104 TNFR-CYS 2.  
 REPEAT 105 141 TNFR-CYS 3.  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 250 AA; 28164 MW; 48477C2E0C244697 CRC64;

Query Match 11.3%; Score 143.5; DB 1; Length 250;  
 Best Local Similarity 25.7%; Pred. No. 1.4e-05; Mismatches 97; Indels 75; Gaps 14;  
 Matches 67; Conservative 22; MisMatches 97; Index 75; GapOpen 14;

QY 3 COFNEWYDQWGRGVTQRCGGPGQELS RDCCGEGGDAYCTACPPRYKSSWGHK--CQS 60  
 Db 27 CPDKHWTGGIC--CRMCRGCFVFKDCEQDRTA-AQCDPCIPGTFSFSPDYHTRPHCES 83  
 Qy 61 CTCAVINRQVNQVNTSNAVCGDCIPLPRVKTRIGLQDQECIPCTKQTPPTSVQCAF 120  
 Db 84 CRHCNSGFLIR--NCTVTAKEC--SSKNNQ--C--CRDQECLC--DPPLNPALTR 130  
 Qy 121 QLSLVEADAPVPP-----QEAQLVALVSS---LLVFT 151  
 Db 131 QPS--ETPSPOPPPTPHGTEPKPSWPLHQLPNSTVYSGRSRSHPLCSSDCIRIVTFS 188  
 Qy 152 LAFLGILFLFLYCKQQFFHRHCOGGGLQFEADKTAKERSLFP--VPPSKETSAESQVSWAPG 209  
 Db 189 SMFL--IFVLGAIFFQRNRHGP---NEDROQAVPEEPCPYSCPREEGSA--- 234  
 Qy 210 SLAQFLSDLSPVPIPOOQGP 230  
 Db 235 -----IPIQEDYRKPE 245

RESULT 6  
 TNR6\_PIG STANDARD; PRT; 332 AA.

ID TNR6\_PIG STANDARD; PRT; 332 AA.  
 AC 077736; 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
 DE TNFRSF6 OR APT1 OR FAS.  
 OS sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiua; Suidae; Sus.  
 OX NCBI\_TaxId=9823;  
 RN [1]

SEQUENCE FROM N.A.  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
 RT "Expression of apoptosis-associated genes in hibernating and stunned myocardiium of pig";  
 RL submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTER MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVATED CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATIC-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTI-GEN STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTER PROTEINS.  
 -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
 -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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 CC or  
 CC  
 DR EMBL; AJ001202; CAA04596; 1; -.  
 DR HSSP; P2545; IDDF.  
 DR InterPro; IPR00488; Death.  
 DR InterPro; IPR01368; TNFR\_C6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00205; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS5007; DEATH\_DOMAIN; 1.  
 DR SIGNAL 1 16 TUMOR NECROSIS FACTOR RECEPTOR CHAIN 17 332  
 FT DOMAIN 17 175 SUPERFAMILY MEMBER 6.  
 FT TRANSMEM 176 192 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 193 332 POTENTIAL.  
 FT REPEAT 45 81 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 82 125 TNFR-CYS 1.  
 FT REPEAT 126 164 TNFR-CYS 2.  
 FT DOMAIN 227 311 DEATH.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 116 116 TNFR-CYS 3.  
 SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682750BF1B CRC64;

Query Match 11.2%; Score 143; DB 1; Length 332;  
 Best Local Similarity 31.2%; Pred. No. 2e-05; Mismatches 53; Indels 20; Gaps 8; Matches 40; Conservative 15; MisMatches 40; Index 18; GapOpen 15; GapClose 15;

QY 2 DCQENEWYDQWGRGVTQRCGGPGQELS KRGCGYBGGDAYCTACPPRRKSSWGHK--KQ 59  
 Db 45 ECPEQSHRE-GQ-FCCQCPGPKRKHAC-TSGAGARQCPVSEGEDYTDKHNHSSCR 100  
 Qy 60 SCITCAVINRQV-KVNQVNTSNAVCGDCIPLPRVKTRIGLQDQECIPCT-----KQ 110  
 Db 101 RCRVQDGEGELEVKNCIRTQTKC-RCKPNFFCHTS---QCEHCNCTCBEHVENC 155  
 Qy 111 TPTSEVQC 118  
 Db 156 TPTSNTKC 163

RESULT 7  
 TR11\_MOUSE STANDARD; PRT; 625 AA.

ID TR11\_MOUSE STANDARD; PRT; 625 AA.  
 AC 03505; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 01-MAR-2002 (Rel. 41, last annotation update)  
 DE tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF- $\kappa$ B) (osteoclast differentiation factor (receptor) (ODFR)).  
 DE TNFRSF11A OR RANK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=petal liver;  
 RX MEDLINE=9803297; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Tepe M.C., Dubose R.F., Cosman D., Galibert L.;  
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RP [2]  
 RP FUNCTION.



FT TRANSMEM 203 223  
 FT DOMAIN 224 283  
 FT REPEAT 42 75  
 FT REPEAT 78 119  
 FT REPEAT 121 162  
 FT DISULFID 42 53  
 FT DISULFID 54 67  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT DISULFID 96 111  
 FT DISULFID 99 119  
 FT DISULFID 121 127  
 FT DISULFID 138 162  
 FT CARBOHYD 110 110  
 FT CARBOHYD 173 173  
 FT CONFLICT 17 17  
 SQ SEQUENCE 283 AA; 30392 MW; 46CE13C270242C1 CRC64;

Query Match 11.1%; Score 141.5; DB 1; Length 283;  
 Best Local Similarity 26.4%; Pred. No. 2.3e-05; Indels 53; Gaps 14;  
 Matches 63; Conservative 98; Mismatches 53; Signal 1;  
 QY 3 CQENEYWQDGRCVTCQRCGPGQQLSKDGMCGYGGDAYCTACPPRKYKSSW-GHMKCQSC 61  
 Db 42 CKEDEVY-PVGSEC--CPKCPSPGYRIVKEACELTG--TVCPCPOTYIHLINGLSKCLQC 96  
 QY 62 ITC- -AVINRVKVNCTATSNAVCDCLP-----RFLV-----RKTRIGG 98  
 Db 97 QMCDFPAMGLRASR-NCSRTENAVCG-CSPGHFCTVQDGDHCAACRAYATSSPGQRVQKG 154  
 QY 99 LQDQE----CIPCKQTPSEVQAFOLS---LYEADATPVPPQEATLVAVLVSLLVF 150  
 Db 155 TESQDTLCQNCPGPFTSPNGTLECOHQTKCSWLVTKAGAGTSSSHWWNWLSSILIVI 214  
 Qy 151 TLAFGLGLFLYCKQFNRHQCGGILQF-----EADTTAKEESLIFVPPSKETSA 200  
 Db 215 VCSTVGL--ITC--VKRRKPERGVKVTVSVORKRQEAEGEATVIEALQAPPVTTVA 268

RESULT 9  
 TNR6\_BOVIN STANDARD; PRT; 323 AA.  
 ID TNR6\_BOVIN  
 AC P51867;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor superfamily member 6 precursor (PASL receptor) (Apoptosis-mediating surface antigen FAS) (apo-1 antigen) (CD95).  
 DE TNFRSF6 OR APT1 OR FAS.  
 OS Bos taurus (Bovine).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Bovine; Bos.  
 OX NCBI\_TaxId=9913;  
 RP [1] SEQUENCE FROM N.A.  
 RX MEDLINE:96016401; PubMed=8634151;  
 RA Yoo J., Stone R.T., Beartie C.W.;  
 RT "Cloning and characterization of the bovine Fas.",  
 RL Cell Biol. 15:227-234 (1996).  
 CC -- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARAGINE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: Contains a death domain involved in the binding of FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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CC -----  
 DR EMBL; U34794; AAC46546\_1;  
 DR HSSP; P2545; IDDF;  
 DR InterPro; IPR00488; Death.  
 DR Prosite; PS50050; TNFR\_NGFR\_2.  
 DR Prosite; PS50017; DEATH\_DOMAIN\_1.  
 DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal; FT SIGNAL 1 16 POTENTIAL  
 DR CHAIN 17 323  
 FT DOMAIN 17 170  
 FT TRANSMEM 171 188  
 FT DOMAIN 189 323  
 FT REPEAT 45 80  
 FT REPEAT 81 124  
 FT DOMAIN 125 163  
 FT REPEAT 238 306  
 SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;

Query Match 10.6%; Score 134.5; DB 1; Length 323;  
 Best Local Similarity 26.2%; Pred. No. 0.00011; Indels 70; Gaps 8;  
 Matches 42; Conservative 19; Mismatches 70; Signal 1;  
 QY 3 CQENEYWQDGRCVTCQRCGPGQQLSKDGMCGYGGDAYCTACPPRKYKSSW-GHMKCQSC 62  
 Db 45 CQEGLYRHO--FCCQRPQPKGNKGK-KRGDDTPCVCVLSSEGNEYTDKSIIHS-DKCI 99  
 QY 63 TCavinrvo---KVNCTATSNAVCDGDLPRFVRKTRIGGLQDQECPCT-----KQ 110  
 Db 100 RSC1DEEHGLEVEQNCTIRTRNKC-RKSNFF---CNNSPEHCNCCTCERHG1IEKC 154  
 QY 111 TPTSEVQCAFOLSLVEADATPVPPQEATLVAVLVSLLVF 150  
 Db 155 TPISNTKCKGSRSHANS-----LWALLILLIPIVLIVY 187

RESULT 10  
 TRIA\_PIG STANDARD; PRT; 461 AA.  
 ID TRIA\_PIG  
 AC P5055;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-RI) (TNF-RI)  
 DE (p55) TNFSF1A OR TNFR1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxId=923;  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE=Kidney;  
 RX MEDLINE:96011645; PubMed=7590278;  
 RA Suter B., Pauli U.H.;  
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.",





RESULT 13

ID TRIB_HUMAN	STANDARD;	PRT;	461 AA.
AC P20333;			
DT 01-FEB-1991 (Rel. 17, Created)			
DT 01-AUG-1991 (Rel. 19, Last sequence update)			
DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TNFR2) (p80) (TNF-R2) (p75) (CD120B) (Etanercept).			
DE TNFRSF1B OR TNFR.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1] SEQUENCE FROM N.A. MEDLINE=90260639; PubMed=2160731;			
RX Dower C.A., Davis T., Anderson D., Solan L., Beckmann M.P., Jerzy R., RT "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins."; Science 248:1019-1023(1990).			
RN [2] SEQUENCE FROM N.A. MEDLINE=9104591; PubMed=2172983;			
RX Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale R.K., Squires C.H., Thompson R.C., Vannice J.L.; RT "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).			
RN [3] SEQUENCE FROM N.A. MEDLINE=9629945; PubMed=8661109;			
RX Beltinger P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslie D., Stallaard B.J., Goeddel D.V., Desauvage F.J., Brodeur G.M.; RT "Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).			
RN [4] SEQUENCE OF 116-461 FROM N.A. AND PARTIAL SEQUENCE. MEDLINE=0349572; Pubmed-2166946;			
RX Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Rinold G.M.; RT "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor"; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).			
RP SEQUENCE OF 27-31. MEDLINE=90110215; PubMed=2153136;			
RX Engelmann H., Novick D., Wallach D.; RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors"; J. Biol. Chem. 265:1531-1536(1990).			
RN [5] SEQUENCE OF 23-40. MEDLINE=91056048; Pubmed=2173696;			
RX MEDLINE=91056048; Pubmed=2173696;			

RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.B., Lesslauer W., Brockhaus M.; "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).

RA Pennica D., Lam V.T., Mizé N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.; "Biochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation"; J. Biol. Chem. 267:21172-21178(1992).

RA [8] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH TRAF2. MEDLINE=99221490; PubMed=10206649;

RX RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; RT "Structural basis for self-association and receptor recognition of human TRAF2"; Nature 398:533-538(1999).

CC CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-BETA. APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES

CC CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immunoglobulin FC chain. It binds to TNF-alpha and blocks its interactions with receptors.

CC CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS

CC CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prowww/ed120b.htm"

CC CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrelinfo.com/".

CC CC -----

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DR EMBL; M32315; AAA59929; 1; -. DR EMBL; M32315; AAA59929; 1; -. DR EMBL; M32315; AAC63362; 1; -. DR EMBL; U52156; AAC50622; 1; JOINED. DR EMBL; U52157; AAC50622; 1; JOINED. DR EMBL; U52158; AAC50622; 1; JOINED. DR EMBL; U52159; AAC50622; 1; JOINED. DR EMBL; U52160; AAC50622; 1; JOINED. DR EMBL; U52161; AAC50622; 1; JOINED. DR EMBL; U52162; AAC50622; 1; JOINED. DR EMBL; U52163; AAC50622; 1; JOINED. DR EMBL; U52164; AAC50622; 1; JOINED. DR EMBL; M55994; AAC36755; 1; -. DR PIR; A3536; A35356. DR PIR; A36007; A36007. DR PIR; A36475; A36475. DR PIR; B35010; B35010. DR PIR; A23666; A23666. DR PDB; ICAG; 12-Apr-99. DR MIM; 191191; -. DR Inter-Pro; IPR001368; TNFR\_c6. DR Pfam; PF00020; TNFR\_c6; 4. DR ProDom; PDB00071; TNFR\_c6; 1. DR SMART; SM00208; TNFR\_4. DR PROSITE; PS00652; TNFR\_NGFR\_1; 2. DR PROSITE; PS50050; TNFR\_NGFR\_2; 4. DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal;





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